## SEQUENCE LISTING

<110> SIREEN AG

 $<\!\!120\!\!>$  Methods of identifying, selecting and/or characterizing compounds which modulate the activity of a Src familiy kinase

<130> SI07P001WO

<150> EP 03028713.0

<151> 2003-12-12

<160> 51

<170> PatentIn version 3.1

<210> 1

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> MISC\_FEATURE

<223> Description of sequence: Src-KA

<400> 1

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg 1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Gly Ala Phe

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg 35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe 50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly 65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu 85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln 100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser 115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp 130 135 140 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu 155 150 145 Ser Glu Arq Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu 165 170 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg 195 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn 210 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu 230 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln 245 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu 265 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr 280 Trp Asn Gly Thr Thr Arg Val Ala Ile Ala Thr Leu Lys Pro Gly Thr Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu 310 315 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro 330 Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe 345 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp 360 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn

395

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405
410
415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val 450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg 465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp 485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe 500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro 515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu 530 535

<210> 2

<211> 536

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Src-TQ

<400> 2

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg 1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe
20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
35 40 45

🖘 Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe

50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu 85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln 100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser 115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp 130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu 145 150 155 160

Ser Glu Arg Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu 165 170 . 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser 180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg 195 200 205

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn 210 220

Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu 225 230 235 240

Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln 245 250 255

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu 260 265 270

Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr 275 280 285

Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr 290 295 300 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu 310 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe 345 Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp 360 Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn 375 Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp 410 Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 425 Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe 505 500 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro 515

<210> 3 <211> 536 <212> PRT

530

Gln Tyr Gln Pro Gly Glu Asn Leu

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Src-YF

<400> 3

Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg 1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe 20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg 35 40 45

Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe 50 55 60

Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly 65 70 75 80

Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu 85 90 95

Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln 100 105 110

Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser 115 120 125

Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp 130 135 140

Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu 145 150 155 160

Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu 165 170 175

Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser 180 185 190

Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg 195 200 205

Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn 210 215 220

Ser 225	Leu	Gln	Gln	Leu	Val 230	Ala	Tyr	Tyr	Ser	Lys 235	His	Ala	Asp	Gly	Leu 240
Cys	His	Arg	Leu	Thr 245	Thr	Val	Cys	Pro	Thr 250		Lys	Pro	Gln	Thr 255	Gln

Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu 260 265 270

Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr 275 280 285

Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr 290 295 300

Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu 305 310 315 320

Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro 325 330 335

Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe 340 . 345 350

Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp 355 360 365

Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn  $370 \hspace{1cm} 375 \hspace{1cm} 380$ 

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn 385  $390 \hspace{1.5cm} 395 \hspace{1.5cm} 400$ 

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp 405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val 450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg

480 470 475 465 Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp 490 Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe 505 Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro 520 515 Gln Phe Gln Pro Gly Glu Asn Leu <210> 4 <211> 536 <212> PRT <213> Homo sapiens <220> <221> misc\_feature <223> Description of sequence: Src-TQ/YF <400> 4 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg 5 Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe 25 Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg 40 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly 75 70 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu 90 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln

Ile Val Asn Asn Thr Glu Gly Asp Trp Leu Ala His Ser Leu Ser 115 120 125

- Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp 130 135 140
- Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu 145 150 155 160
- Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu 165 170 175
- Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser 180 185 190
- Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg 195 200 205
- Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn 210 220
- Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu 225 230 235
- Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln 245 250 255
- Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu 260 265 270
- Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr 275 280 285
- Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr 290 295 300
- Met\_Ser\_Pro\_Glu\_Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu 305 310 315 320
- Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro 325 330 335
- Ile Tyr Ile Val Glu Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe 340 345 350
- Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp 355 360 365
- Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn 370 380

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn 385 390 395 400

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val 450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg 465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp 485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe 500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro 515 520 525

Gln Phe Gln Pro Gly Glu Asn Leu

<210> 5

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Yes-KA

<400> . 5

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr 1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr 20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
35 40 45

- Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly 50 55 60
- Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val 65 70 75 80
- Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe 85 90 95
- Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe 100 105 110
- Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp 115 120 125
- Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser 130 135 140
- Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe 145 150 155 160
- Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly 165 170 175
- Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly 180 185 190
- Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn 195 200 205
- Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile 210 215 220
- Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr 225 230 235 240
- Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro 245 250 255
- Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile 260 265 270
- Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe 275 280 285
- Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile

300 295 290 Ala Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu 310 315 305 Ala Gln Ile Met Lys Lys Leu Arg His. Asp Lys Leu Val Pro Leu Tyr 330 Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser 345 Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met 375 Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 390 395 Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly 405 410 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala 425 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg 440 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu 475 470 Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly 490 Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp 505 Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp 520 Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu 540 535

<210> 6 <211> 543 <212> PRT <213> Homo sapiens <220> <221> misc\_feature <223> Description of sequence: Yes-TQ <400> 6 Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr 25 Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys 40 Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val 70 Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe 90 Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe 105 Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp 120 115 Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser 135 130 Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe 145 Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Asn Pro Gly 170 165

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
195 200 205

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile 210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr 225 230 235 240

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro 245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile 260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe 275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile 290 295 300

Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu 305 310 315 320

Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr 325 330 335

Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe Met Ser 340 345 350

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu 355 360 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met 370 380

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 385 390 395 400

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly 405 410 415

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala 420 425 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg 435 440 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu 450 455 460 Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu 465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp 500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp 515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu 530 540

<210> 7

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Yes-YF

<400> 7

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr 1  $\phantom{\bigg|}$  5  $\phantom{\bigg|}$  10  $\phantom{\bigg|}$  15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr 20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys 35 40 45

Gla The Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly 50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe 85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe 100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp

125 120 115 Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser 135 140 130 Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe 150 155 Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Asn Pro Gly 170 165 Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly 185 180 Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn 200 · 195 Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile 215 Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr 235 230 Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro 250 Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile 265 Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe 280 Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile 295 Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu 315 310 Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr 330 Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu 355 360 365 Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met 370 . 375 380

Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 385 390 395 400

Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
405 410 415

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala 420 425 430

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
435 440 445

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu 450 460

Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu 465 470 475 480

Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly 485 490 495

Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp 500 505 510

Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp 515 520 525

Tyr Phe Thr Ala Thr Glu Pro Gln Phe Gln Pro Gly Glu Asn Leu 530 540

<210> 8

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Yes-TQ/YF

<400> 8

Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr 1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr 20 25 30

- Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys 35 40 45
- Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly 50 55 60
- Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val 65 70 75 80
- Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe 85 90 95
- Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe 100 105 110
- Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp 115 120 125
- Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser 130 135 140
- Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe 145 150 155 160
- Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Asn Pro Gly 165 170 175
- Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn 195 200 205
- Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile 210 215 220
- Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr 225 230 235 240
- Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro 245 250 255
- Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile 260 265 270
- Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe 275 280 285

- Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile 290 295 300
- Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu 305 310 315 320
- Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr 325 330 335
- Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe Met Ser 340 345 350
- Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu 355 360 365
- Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met 370 375 380
- Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 385 390 395 400
- Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly 405 410 415
- Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala 420 425 430
- Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg 435 440 445
- Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu 450 455 460
- Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu 465 470 475 480
- Val Leu Glu Glu Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly 485 490 495
- Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp 500 505 510
- Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp 515 520 525
- Tyr Phe Thr Ala Thr Glu Pro Gln Phe Gln Pro Gly Glu Asn Leu

530 535 540

<210> 9

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fgr-KA

<400> 9

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys

1 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp 20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala 35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly 50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr 65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly 100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile 115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp 130 · 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser 145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr 165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly
180 185 190

- Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr 195 200 205
- Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln 210 215 220
- His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro 225 230 235 240
- Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp
  245 250 255
- Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly 260 265 270
- Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val 275 280 285
- Ala Val Ala Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu 290 295 300
- Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln 305 310 315 320
- Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe 325 330 335
- Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln 340 345 350
- Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu 355 360 365
- Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg 370 375 380
- Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp 385 390 395. 400
- Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln 405 410 415
- Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe 420 425 430
- Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys 450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro 465 470 475 .480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg 485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu 500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln 515 520 525

Thr

<210> 10

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fgr-TQ

<400> 10

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys 1  $\phantom{\bigg|}$  5  $\phantom{\bigg|}$  10  $\phantom{\bigg|}$  15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp 20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala 35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly 50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr 65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
100 105 110

- Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile 115 120 125
- Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp 130 135 140
- Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser 145 . 150 . 155 . 160
- Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr
- Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly
  180 185 190
- Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr 195 200 205
- Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln 210 215 220
- His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro 225 230 230 235
- Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp 245 250 255
- Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly
  260 265 270
- Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val 275 280 285
- Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser 🚉 Ala Phe Leu 290 295 300
- Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln 305 310 315 320
- Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe 325 330 335
- Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln 340 345 350
- Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu

355 360 365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg 370 375 380

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp 385 390 395 400

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln 405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe
420 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys 450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro 465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg 485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu 500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln 515 520 525

Thr

<210> 11

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fgr-YF

<400> 11

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys 1 5 10 15

- Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp 20 · 25 30
- His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala 35 40 45
- His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly 50 55 60
- Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr 65 70 75 80
- Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu 85 90 95
- Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
  100 105 110
- Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile 115 120 125
- Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp 130 135 140
- Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser 145 150 155 160
- Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr 165 170 175
- Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly 180 185 190
- Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr 195 200 205
- Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln 210 215 220
- His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro 225 230 235 240
- Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp 245 250 255
- Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly
  . 260 265 270

- Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val 275 280 285
- Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu 290 295 300
- Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln 305 310 315 320
- Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe 325 330 335
- Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln 340 345 350
- Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu 355 360 365
- Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg 370 375 380
- Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp 385 390 395 400
- Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln 405 410 415
- Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe 420 425 430
- Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 435 440 445
- Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys
  455
  460
- Arg\_Glu Val\_Leu\_Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro 465 470 475 480
- Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg
  485 490 495
- Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu 500 505 510
- Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Phe Gln Pro Gly Asp Gln
  515 520 525

Thr

<210> 12

<211> 529

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fgr-TQ/YF

<400> 12

Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
1 5 10 15

Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp 20 25 30

His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala 35 40 45

His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly 50 55 60

Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr 65 70 75 80

Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly 100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ger Ger Gly Cys Ile 115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp 130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser 145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr 165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly

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185 190 180 Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr 200 Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro 225 230 Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly 260 265 Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val 280 Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln 315 310 Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Gln Glu Phe 330 Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln 345 Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu 360 355 Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg 375 Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp 395 Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe 425

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys 450 455 460

Arg.Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro 465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg 485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu 500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Phe Gln Pro Gly Asp Gln 515 520 525

Thr

<210> 13

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fyn-KA

<400> 13

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu 1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr 20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro 35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe 50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly 65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg 85 90 95

- Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu 100 105 110
- Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
  115 120 125
- Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile 130 135 140
- Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu 145 150 155 160
- Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg 165 170 175
- Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp 180 185 190
- Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu 195 200 205
- Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu 210 215 220
- Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys 225 230 235 240
- Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu 245 250 255
- Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln 260 265 270
- Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly 275 280 285
- Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Ala Thr Leu Lys Pro Gly 290 295 300
- Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys 305 310 315 320
- Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu 325 330 335
- Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp 340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val 355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met 370 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn 385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu 405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp 420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp 435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg 450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu 465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His 485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr 500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu 515 520 525

Pro Gln Tyr Gln Pro Gly Glu Asn Leu 530 535

<210> 14

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fyn-TQ

<400> 14

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu

10 15 1 5 Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr 30 20 Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly 120 Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile 135 Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu 155 Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp 185 Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu

- Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln 260 265 270
- Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly 275 280 285
- Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly 290 295 300
- Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys 305 310 315 320
- Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu 325 330 335
- Pro Ile Tyr Ile Val Gln Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp 340 345 350
- Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val 355 360 365
- Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met 370 380
- Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn 385 390 395 400
- Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu 405 410 415
- Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp 420 425 430
- Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp 435 440 445
- Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg 450 460
- Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu 465 470 475 480
- Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His 485 490 495
- Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr 500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu 515 520 525

Pro Gln Tyr Gln Pro Gly Glu Asn Leu 530 535

<210> 15

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fyn-YF

<400> 15

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu 1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr 20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro 35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe 50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly 65 70 75 80

Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg 85 90 95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu 100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly 115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile 130 135 140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu 145 150 155 160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg 165 170 175 Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp 180 185 190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu 195 200 205

Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu 210 215 220

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys 225 230 235 240

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu 245 250 255

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln 260 265 270

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly 275 280 285

Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly 290 295 300

Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys 305 310 315 320

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu 325 330 335

Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp 340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Ler 3-0 Asn Leu Val 355 360

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met 370 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn 385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp

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420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp 435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg 450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu 465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr 500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu 515 520 525

Pro Gln Phe Gln Pro Gly Glu Asn Leu 530 535

<210> 16

<211> 537

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Fyn-TQ/YF

<400> 16

Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu 1 5 10 15

Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr 20 25 30

Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro 35 40 45

Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe 50 55 60

Gly Gly Val Asn Ser Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly 65 70 75 80

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Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg 85 90 95

Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu 100 105 110

Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
115 120 125

Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile 130 135 140

Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu 145 150 155 160

Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg 165 170 175

Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp 180 185 190

Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu 195 200 205

Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu 210 215 220

Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys 225 230 235 240

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu 245 250 255

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln 260 265 270

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly 275 280 285

Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly 290 295 300

Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys 305 310 315 320

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
325 330 335

Pro Ile Tyr Ile Val Gln Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp 340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val 355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met 370 375 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn 385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu 405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp 435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg 450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu 465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His 485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr 500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu  $\frac{\pi}{50.5}$  520 525

Pro\_Gln Phe\_Gln\_Pro Gly Glu Asn Leu 530 535

<210> 17

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lck-KA

<400> 17

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn 1 5 . 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly 20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu 35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn 50 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu 65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu 85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro 100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe 115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro 130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala 145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu 165 170 175

Val Val Lys His Tyr Lys Ile Arg Ass 190 Phe Tyr 180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His 195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys 210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val 225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe

				245					250					255	
Gly	Glu	Val	Trp 260	Met	Gly	Tyr	Tyr	Asn 265	Gly	His	Thr	Lys	Val 270	Ala	Val
Ala	Ser	Leu 275	Lys	Gln	Gly	Ser	Met 280	Ser	Pro	Asp	Ala	Phe 285	Leu	Ala	Glu
Ala	Asn 290	Leu	Met	Lys	Gln	Leu 295	Gln	His	Gln	Arg	Leu 300	Val	Arg	Leu	Tyr
Ala 305	Val	Val	Thr	Gln	Glu 310	Pro	Ile	Tyr	Ile	Ile 315	Thr	Glu	Tyr	Met	Glu 320
Asn	Gly	Ser	Leu	Val 325	Asp	Phe	Leu	Lys	Thr 330	Pro	Ser	Gly	Ile	Lys 335	Leu
Thr	Ile	Asn	Lys 340	Leu	Leu	Asp	Met	Ala 345	Ala	Gln	Ile	Ala	Glu 350	Gly	Met
Ala	Phe	Ile 355	Glu	Glu	Arg	Asn	Tyr 360	Ile	His	Arg	Asp	Leu 365	Arg	Ala	Ala
Asn	Ile 370	Leu	Val	Ser	Asp	Thr 375	Leu	Ser	Суз	Lys	Ile 380	Ala	Asp	Phe	Gly
Leu 385	Ala	Arg	Leu	Ile	Glu 390	Asp	Asn	Glu	Tyr	Thr 395	Ala	Arg	Glu	Gly	Ala 400
Lys	Phe	Pro	Ile	Lys 405		Thr	Ala	Pro	Glu 410		Ile	Asn	Tyr	Gly 415	Thr
Phe	Thr	Ile	Lys 420		Asp	Val	Trp	Ser 425		Gly	Ile	Leu	Leu 430		Glu
Ile	Val	Thr 435		Gly	Arg	Ile	Pro 440		Pro	Gly	Met	Thr 445	Asn	Pro	Glu
Val	Ile 450		Asn	Leu	Glu	Arg 455		Tyr	Arg	Met	Val 460	Arg	Pro	Asp	Asn
Cys 465		Glu	Glu	Leu	Tyr 470		Leu	Met	Arg	Leu 475		Trp	Lys	Glu	480
Pro	Glu	Asp	Arg	Pro 485		Phe	Asp	Tyr	Leu 490		Ser	Val	. Leu	Glu 495	

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro 500 505

<210> 18

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lck-TQ

<400> 18

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn 1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly 20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu 35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn 50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu 65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu 85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro 100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe 115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro 130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala 145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu 165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr 180 185 190 Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys 210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Glu Asp Glu Trp Glu Val 225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe 245 250 255

Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val 260 265 270

Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu 275 280 285

Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr 290 295 300

Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Gln Glu Tyr Met Glu 305 310 315 320

Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu 325 330 335

Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met 340 345 350

Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 355 360 365

Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly 370 375 380

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr 405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu 420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn 450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg 465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp 485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro 500

<210> 19

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lck-YF

<400> 19

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn 1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly 20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu 35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn 50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu 65 70 75 80

Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu 85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe 115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro

130 135 140 Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala 145 150 Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu 170 Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr 185 Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe 250 Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu 315 310 Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu 330 Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly

375

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr 405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu 420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu 435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn 450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg 465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp 485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Phe Gln Pro Gln Pro 500 505

<210> 20

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lck-TQ/YF

<400> 20

Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn 1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly 20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu 35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn 50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu 65 70 75 80

- Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu 85 90 95
- Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro 100 105 110
- Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe 115 120 125
- Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro 130 135 140
- Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala 145 150 155 160
- Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu 165 170 175
- Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr 180 185 190
- Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His 195 200 205
- Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys 210 215 220
- Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val 225 230 235 240
- Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe 245 250 255
- Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val 260 265 270
- Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu 275 280 285
- Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr 290 295 300
- Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Gln Glu Tyr Met Glu 305 310 315 320
- Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu 325 330 335

Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met 340 345 350

Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 355 360 365

Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly 370 375 380

Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 385 390 395 400

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr 405 410 415

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu 420 425 430

Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu 435 440 445

Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn 450 455 460

Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg 465 470 475 480

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp 485 490 495

Phe Phe Thr Ala Thr Glu Gly Gln Phe Gln Pro Gln Pro 500 505 :

<210> 21

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Hck-KA

<400> 21

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu  $1 ag{10}$  5 10 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly

20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro 35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser 50 . 55 60

His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile 65 70 75 80

Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu 85 90 95

Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu 100 105 110

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro 115 120 125

Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe 130 135 140

Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro 145 150 155 160

Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys 165 170 175

Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp 180 185 190

Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr 195 200 205

Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His 210 215 220

Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys 225 230 235 240

Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile 245 250 255

Pro Arg Glu Ser Leu Lys Leu Glu Lys Leu Gly Ala Gly Gln Phe 260 265 270

- Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val 275 280 285
- Ala Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu 290 295 300
- Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His 305 310 315
- Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala 325 330 335
- Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln 340 345 350
- Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met 355 360 365
- Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 370 375 380
- Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly 385 390 395 400
- Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 405 410 415
- Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser 420 425 430
- Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu 435 440 445
- Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu 450 455 460
- Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn 465 470 475 480
- Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg 485 490 495
- Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp 500 505 510
- Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro 515 520 525

<210> 22 <211> 525 <212> PRT <213> Homo sapiens												
<220> <221> misc_feature <223> Description of sequence: Hck-TQ												
<400> 22												
Gly Gly Arg Ser Ser Cys 1 5	Glu Asp Pro Gly 10	Cys Pro Arg	Asp Glu Glu 15									
Arg Ala Pro Arg Met Gly 20	Cys Met Lys Ser	Lys Phe Leu	Gln Val Gly 30									
Gly Asn Thr Phe Ser Lys 35	Thr Glu Thr Ser 40	: Ala Ser Pro 45	His Cys Pro .									
Val Tyr Val Pro Asp Pro	Thr Ser Thr Ile	E Lys Pro Gly 60	Pro Asn Ser									
His Asn Ser Asn Thr Pro	o Gly Ile Arg Glu	ı Ala Gly Ser 75	Glu Asp Ile 80									
Ile Val Val Ala Leu Ty 85	Asp Tyr Glu Ala 90	a Ile His His	Glu Asp Leu 95									
Ser Phe Gln Lys Gly Asp 100	o Gln Met Val Va 105	l Leu Glu Glu	Ser Gly Glu 110									
Trp Trp Lys Ala Arg Sen	r Leu Ala Thr Ard	g Lys Glu Gly 125										
Ser Asn Tyr Val Ala Aro	y Val Asp Ser Le 135	ı Glu Thr Glu 140	Glu Trp Phe									
Phe Lys Gly Ile Ser Are		ı Arg Gln Leu 155	Leu Ala Pro 160									
Gly Asn Met Leu Gly Se 165	r Phe Met Ile Are		Thr Thr Lys 175									
Gly Ser Tyr Ser Leu Se: 180	r Val Arg Asp Ty 185	r Asp Pro Arg	Gln Gly Asp 190									

Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr 195 200 205

- Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His 210 215 220
- Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys 225 230 . 235 240
- Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile 245 250 255
- Pro Arg Glu Ser Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe 260 265 270
- Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val 275 280 285
- Ala Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu 290 295 300
- Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His 305 310 315
- Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Gln Glu Phe Met Ala 325 330 335
- Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln 340 345 350
- Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met 355 360 365
- Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 370 375 380
- Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 405 410 415
- Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser 420 425 . 430
- Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu 435 440 445
- Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu

450 455 460 Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn 470 465 475 Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp 505 Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro 520 .<210> 23 <211> 525 <212> PRT <213> Homo sapiens <220> <221> misc\_feature <223> Description of sequence: Hck-YF <400> 23 Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly 25 Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro 115 120 125

Ser	Asn 130	Tyr	Val	Ala	Arg	Val 135	Asp	Ser	Leu	Glu	Thr 140	Glu	Glu	Trp	Phe
Phe 145	Lys	Gly	Ile	Ser	Arg 150	Lys	Asp	Ala	Glu	Arg 155	Gln	Leu	Leu	Ala	Pro 160
Gly	Asn	Met	Leu	Gly 165	Ser	Phe	Met	Ile	Arg 170	Asp	Ser	Glu	Thr	Thr 175	Lys
Gly	Ser	Tyr	Ser 180	Leu	Ser	Val	Arg <sub>.</sub>	Asp 185	Tyr	Asp	Pro	Arg	Gln 190	Gly	Asp
Thr	Val	Lys 195	His	Tyr	Lys	Ile	Arg 200	Thr	Leu	Asp	Asn	Gly 205	Gly	Phe	Tyr
Ile	Ser 210	Pro	Arg	Ser	Thr	Phe 215	Ser	Thr	Leu	Gln	Glu 220	Leu	Val	Asp	His
<b>T</b> yr 225	Lys	Lys	Gly	Asn	Asp 230	Gly	Leu	Cys	Gln	Lys 235	Leu	Ser	Val	Pro	Cys 240
Met	Ser	Ser	Lys	Pro 245	Gln	Lys	Pro	Trp	Glu 250	Lys	Asp	Ala	Trp	Glu 255	Ile
Pro	Arg	Glu	Ser 260	Leu	Lys	Leu	Glu	Lys 265	Lys	Leu	Gly	Ala	Gly 270	Gln	Phe
Gly	Glu	Val 275	Trp	Met	Ala	Thr	Tyr 280	Asn	Lys	His	Thr	Lys 285	Val	Ala	Val
Lys	Thr 290	Met	Lys	Pro	Gly	Ser 295	Met	Ser	Val	Glu	Ala 300	Phe	Leu	Ala	Glu
Ala 305	Asn	Val	Met	Lys	Thr 310	Leu	Gln	His	Asp	Lys 315	Leu	Val	Lys	Leu	His 320
Ala	Val	Val	Thr	Lys 325	Glu	Pro	Ile	Tyr	Ile 330	Ile	Thr	Glu	Phe	Met 335	Ala
Lys	Gly	Ser	Leu 340	Leu	Asp	Phe	Leu	Lys 345	Ser	Asp	Glu	Gly	Ser 350	Lys	Gln
Pro	Leu	Pro 355	Lys	Leu	Ile	Asp	Phe 360	Ser	Ala	Gln	Ile	Ala 365	Glu	Gly	Met

Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala

380

375

370

Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly 385 390 395 400

Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 405 410 415

Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser 420 425 430

Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu
435 440 445

Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu 450 455 460

Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn 465 470 475 480

Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg 485 490 495

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp 500 505 510

Phe Tyr Thr Ala Thr Glu Ser Gln Phe Gln Gln Gln Pro 515 520 525

<210> 24

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Hck-TQ/YF

<400> 24

Gly Gly Arg Ser Ser Cys Glu Asp Pro Gly Cys Pro Arg Asp Glu Glu
1 5 10 15

Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly 20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro 35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser 50 55 60 His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile 65 70 75 80

Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu 85 90 95

Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu 100 105 110

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro 115 120 125

Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe 130 135 140

Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro 145 150 155 160

Gly Asn Met Leu Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys 165 170 175

Gly Ser Tyr Ser Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp 180 185 190

Thr Val Lys His Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr 195 200 205

Ile Ser Pro Arg Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His 210 215 220

Tyr Lys Lys Gly Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys 225 230 235

Met Ser Ser Lys Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile 245 250 255

Pro Arg Glu Ser Leu Lys Leu Glu Lys Leu Gly Ala Gly Gln Phe 260 265 270

Gly Glu Val Trp Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val 275 280 285

Lys Thr Met Lys Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu 290 295 300

Ala Asn Val Met Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His

320 315 305 310 Ala Val Val Thr Lys Glu Pro Ile Tyr Ile Ile Gln Glu Phe Met Ala 330 Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln 340 Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala 375 Asn Ile Leu Val Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 410 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu 440 Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu 455 Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn 470 Cys Pro Glu Glu Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp 500 505 Phe Tyr Thr Ala Thr Glu Ser Gln Phe Gln Gln Gln Pro 520 <210> 25 <211> 511 <212> PRT <213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lyn-KA

<400> 25

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr 20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His 85 90 . 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu 115 · 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu 130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr 145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His 165 170 '175

Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly
180 185 190

Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile 195 200 205

Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys 210 215 220

Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp 225 230 235 240

- Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly
  245 250 255
- Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val 260 265 270
- Ala Val Ala Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu 275 280 285
- Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg 290 295 300
- Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu 305 310 315 320
- Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly 325 330 335
- Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu 340 345 350
- Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg 355 360 365
- Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp 370 375 380
- Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu 385 390 395 400
- Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe 405 410 . 415
- Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 420 425 430
- Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn 435 440 445
- Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val 450 455 460
- Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys 465 470 475 480
- Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu 485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Pro 500 505 510

<210> 26

<211> 511

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lyn-TQ

<400> 26

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly 1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Les The Glu Glu
115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu 130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr 145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
165 170 175

Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly

185 180 190 Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile 195 200 Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys 215 Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp 230 235 Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val 265 Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu 280 Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg 295 Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Gln Glu Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg 360 Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu 395 Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe

Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 420 425 430

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn 435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val 450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys 465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu 485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro 500 505 510

<210> 27

<211> 511

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lyn-YF

<400> 27

Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly 1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr 20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His 85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe . 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu 115 120 125

- Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu 130 135 140
- Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr 145 150 155 160
- Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His 165 170 175
- Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly 180 185 190
- Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile 195 200 205
- Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys 210 215 220
- Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp 225 230 235 240
- Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly
  245 250 255
- Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val 260 265 270
- Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu 275 280 285
- Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg 290 295 300
- Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu 320
- Tyr\_Met Ala\_Lys\_Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly 325 330 335
- Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu 340 345 350
- Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg 355 360 365
- Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp 370 375 380

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu 385 390 395 400

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe 405 410 415

Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 420 425 430

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn 435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val 450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys 465 470 475

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu 485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Phe Gln Gln Pro 500 505 510

<210> 28

<211> 511

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Lyn-TQ/YF

<400> 28

Met Gly Cys Ile Lys Ser Lys Gly Lys Ser Ser Ser Asp Gly
1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr 20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp

70 . 75 80 65 Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His 85 Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe 100 105 Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu 120 Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly 185 Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp 235 Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val 265 Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu 280 Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Gln Glu 310 315

Tyr Met Ala Lys Gly Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly Gly 325 330 335

Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu 340 345 350

Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu Arg 355 360 365

Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala Asp 370 375 380

Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu 385 390 395 400

Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe 405 410 415

Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu 420 425 430

Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr Asn 435 440 445

Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg Val 450 455 460

Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp Lys 465 470 475 480

Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu 485 490 495

Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Phe Gln Gln Pro 500 505 510

<210> 29

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: BLK-KA

<400> 29

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys 1 5 10 15

- Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp 20 25 30
- Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr 35 40 45
- Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val 50 55 60
- Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu 65 70 75 80
- Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu 85 90 95
- Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe 100 105 110
- Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser 115 120 125
- Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys 130 135 140
- Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe 145 150 155 160
- Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His 165 170 175
- Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg 180 185 190
- Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys 195 200 205
- Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala 210 215 220
- Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser 225 230. 235 240
- Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp 245 250 255
- Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Ala Thr Leu Lys 260 265 270

Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met 275 280 285

Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr 290 295 300

Lys Glu Pro Ile Tyr Ile Val Thr Glu Tyr Met Ala Arg Gly Cys Leu 305 310 315 320

Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg 325 330 335 .

Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu
340 345 350

Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val 355 360 365

Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile 370 375 380

Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys 385 390 395 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala 405 410 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly 420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu 435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu 450 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg 465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala 485 490 495

Thr Glu Arg Gln Tyr Glu Leu Gln Pro 500 505 <211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: BLK-TQ

<400> 30

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys 1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp 20 . 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr 35 40 45

Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val 50 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu 65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu 85 90 95

Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe 100 105 110

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser 115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys 130 135 140

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe 145 150 155 160

Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His 165 170 175

Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg 180 185 190

Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys 195 200 205

- Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala 210 215 220
- Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser 225 230 235 240
- Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp 245 250 255
- Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys 260 265 270
- Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met 275 280 285
- Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr 290 295 300
- Lys Glu Pro Ile Tyr Ile Val Gln Glu Tyr Met Ala Arg Gly Cys Leu 305 310 315 320
- Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg 325 330 335
- Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu 340 345 350
- Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val 355 360 365
- Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile 370 375 380
- Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys 385 390 395 400
- Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala
  405 \_\_\_410\_\_ 415
- Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly
  420 425 430
- Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu
  435 440 445
- Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg 465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala 485 490 495

Thr Glu Arg Gln Tyr Glu Leu Gln Pro 500 505

<210> 31

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: BLK-YF

<400> 31

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys 1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp 20 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr 35 40 45

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val 50 55 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu 65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu 85 90 95

Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe 100 105 110

Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser 115 120 125

Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys 130 135 140

Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe 145 150 155 160

- Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His 165 170 . 175
- Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg 180 185 190
- Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys
  195 200 205
- Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala 210 215 220
- Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser 225 230 235 240
- Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp 245 250 255
- Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys 260 265 270
- Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met 275 280 285
- Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr 290 295 300
- Lys Glu Pro Ile Tyr Ile Val Thr Glu Tyr Met Ala Arg Gly Cys Leu 305 310 315 320
- Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg 325 330 335
- Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu 340 345 350
- Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val 355 360 365
- Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile 370 375 380
- Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys 385 390 395 400
- Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala

405 410 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly
420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu 435 440 445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg 465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala 485 490 495

Thr Glu Arg Gln Phe Glu Leu Gln Pro 500 505

<210> 32

<211> 505

<212> PRT

<213> Homo sapiens

<220>

<221> misc\_feature

<223> Description of sequence: Blk-TQ/YF

<400> 32

Met Gly Leu Val Ser Ser Lys Lys Pro Asp Lys Glu Lys Pro Ile Lys 1 5 10 15

Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp
20 25 30

Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr 35 40 45

Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val 50 55 60

Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu 65 70 75 80

Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu 85 90 95

- Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe 100 105 110
- Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser 115 120 125
- Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys 130 135 140
- Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe 145 150 155 160
- Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His 165 170 175
- Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg 180 185 190
- Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys 195 200 205
- Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala 210 215 220
- Pro Gln Asn Pro Trp Ala Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser 225 230 235 240
- Leu Arg Leu Val Arg Lys Leu Gly Ser Gly Gln Phe Gly Glu Val Trp 245 250 255
- Met Gly Tyr Tyr Lys Asn Asn Met Lys Val Ala Ile Lys Thr Leu Lys 260 265 270
- Glu Gly Thr Met Ser Pro Glu Ala Phe Leu Gly Glu Ala Asn Met Met 275 280 285
- Lys Ala Leu Gln His Glu Arg Leu Val Arg Leu Tyr Ala Val Val Thr 290 · 295 300
- Lys Glu Pro Ile Tyr Ile Val Gln Glu Tyr Met Ala Arg Gly Cys Leu 305 310 315 320
- Leu Asp Phe Leu Lys Thr Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg 325 330 335
- Leu Ile Asp Met Ser Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu 340 345 350

Arg Met Asn Ser Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val 355 360 365

Ser Glu Ala Leu Cys Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile 370 375 380

Ile Asp Ser Glu Tyr Thr Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys 385 390 395 400

Trp Thr Ala Pro Glu Ala Ile His Phe Gly Val Phe Thr Ile Lys Ala 405 410 415

Asp Val Trp Ser Phe Gly Val Leu Leu Met Glu Val Val Thr Tyr Gly 420 425 430

Arg Val Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Asn Leu
435
440
445

Glu Arg Gly Tyr Arg Met Pro Arg Pro Asp Thr Cys Pro Pro Glu Leu 450 455 460

Tyr Arg Gly Val Ile Ala Glu Cys Trp Arg Ser Arg Pro Glu Glu Arg 465 470 475 480

Pro Thr Phe Glu Phe Leu Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala 485 490 495

Thr Glu Arg Gln Phe Glu Leu Gln Pro 500 505

<210> 33

<211> 536

<212> PRT

<213> Chicken

<221> misc\_feature

<223> Description of sequence: Yrk-KA

<400> 33

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly

1 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro 20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn 35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro 50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly 65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr 85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn 100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala 115 120 125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln 130 135 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg 145 150 155 160

Gln Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu 165 170 175

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp 180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp 195 200 205

Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln 210 215 220

Gln Leu Val Gln His Tyr Ile Glu Arr 31- 11- Cys Cys Arg 225 230 235 240

Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser 245 250 255

Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu 260 265 270

Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr 275 280 285

Trp Asn Gly Thr Thr Lys Val Ala Val Ala Thr Leu Lys Pro Gly Thr

295 300 290 Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu 310 Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro 330 Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp 355 Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn 390 Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val 440 Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg 470 Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp 490

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe 500 Tyr Leu Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Asp Asn Gln

<210>	34
<211>	536
<212>	PRT
<213>	Chicken
	-
<220>	
<221>	misc_feature
<223>	Description of sequence: Yrk-TQ

<400> 34

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly
1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn 35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro 50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly 65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr 85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn 100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala 115 120 125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln 130 135 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg 145 150 155 160

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu 165 170 175

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp 180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp 195 200 205

- Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln 210 215 220
- Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg 225 230 235 240
- Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser 245 250 255
- Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu 260 265 270
- Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr 275 280 285
- Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr 290 295 300
- Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu 305 310 315 320
- Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro 325 330 335
- Ile Tyr Ile Val Gln Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe 340 345 350
- Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp 355 360 365
- Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn 370 375 380
- Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn 385 390 395 400
- Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp 405 410 415
- Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 420 425 430
- Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val 435 440 445
- Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
  450 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg 465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp 485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe 500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro 515 520 525

Gln Tyr Gln Pro Gly Asp Asn Gln 530 535

<210> 35

<211> 536

<212> PRT

<213> Chicken

(

<220>

<221> misc\_feature

<223> Description of sequence: Yrk-YF

<400> 35

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly 1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro 20 25 30

Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn 35 40 45

Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro 50 55 60

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly 65 70 75 80

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr 85 90 95

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn 100 105 110

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala

115 120 125

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln 130 135 140

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg 145 150 155 160

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu 165 170 175

Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp 180 185 190

Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp 195 200 205

Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln 210 215 220

Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg 225 . 230 . 235 . 240

Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser 245 250 255

Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu 260 265 270

Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr 275 280 285

Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr 290 295 300

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu 305 310 315 320

Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro 325 330 335

Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe 340 345 350

Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp 355 360 365

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn 370 375 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn 385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp 405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val 450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Glu Val Glu Arg
465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp 485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe 500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro 515 520 525

Gln Phe Gln Pro Gly Asp Asn Gln 530 535

<210> 36

<211> 536

<212> PRT

<213> Chicken

<220>

<221> misc\_feature

<223> Description of sequence: Yrk-TQ/YF

<400> 36

Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly 1 5 10 15

Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
20 25 30

- Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn 35 40
- Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro 50 55 60
- Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly 65 70 75 80
- Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr 85 90 95
- Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn 100 105 110
- Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala 115 120 125
- Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln 130 135 140
- Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg 145 150 155 160
- Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu 165 170 175
- Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp 180 185 190
- Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp 195 200 205
- Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln 210 220
- Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg 225 230 235 240
- Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser 245 250 255
- Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu 260 265 270
- Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr 275 280 285

Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr 290 295 300

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu 305 310 315 320

Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro 325 330 335

Ile Tyr Ile Val Glu Glu Phe Met Ser Glu Gly Ser Leu Leu Asp Phe 340 345 350

Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp 355 360 365

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn 370 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn 385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp 405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr 420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val 450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Glu Val Glu Arg
465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp 485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe 500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro 515 520 525

Gln Phe Gln Pro Gly Asp Asn Gln

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Asp	Phe	Asp 195		Ala	Lys	Gly	Leu 200	Asn	Val	Lys	His	Tyr 205	Lys	Ile	Arg
Lys	Leu 210	Asp	Ser	Gly	Gly	Phe 215	Tyr	Ile	Thr	Ser	Arg 220	Thr	Gln	Phe	Asn
Ser 225	Leu	Gln	Gln	Leu	Val 230	Ala	Tyr	Tyr	Ser	Lys 235	His	Ala	Asp	Gly	Leu 240
Суз	His	Arg	Leu	Thr 245	Thr	Val	Cys	Pro	Thr 250	Ser	Lys	Pro	Gln	Thr 255	Gln
Gly	Leu	Ala	Lys 260	Asp	Ala	Trp	Glu	Ile 265	Pro	Arg	Glu	Ser	Leu 270	Arg	Leu
Glu	Val	Lys 275	Leu	Gly	Gln	Gly	Cys 280	Phe	Gly	Glu	Val	Trp 285	Met	Gly	Thr
Trp	Asn 290	Gly	Thr	Thr	Arg	Val 295	Ala	Ile	Lys	Thr	Leu 300	Lys	Pro	Gly	Thr
Met 305	Ser	Pro	Glu	Ala	Phe 310	Leu	Gln	Glu	Ala	Gln 315	Val	Met	Lys	Lys	Leu 320
Arg	His	Glu	Lys	Leu 325	Val	Gln	Leu	Tyr	Ala 330	Val	Val	Ser	Glu	Glu 335	Pro
Ile	Tyr	Ile	Val 340	Thr	Glu	Tyr	Met	Ser 345	Lys	Gly	Ser	Leu	Leu 350	Asp	Phe
Leu	Lys	Gly 355	Glu	Thr	Gly	Lys	Tyr 360	Leu	Arg	Ļeu	Pro	Gln 365	Leu	Val	Asp
Met	Ala 370	Ala	Gln	Ile	Ala	Ser 375	Gly	Met	Ala	Tyr	Val 380	Glu	Arg	Met	Asn
Tyr 385	Val	His	Arg	Asp	Leu 390	Arg	Ala	Ala	Asn	Ile 395		Val	Gly	Glu	Asn 400
Leu	Val	Cys	Lys	Val 405		Asp	Phe	Gly	Leu 410		Arg	Leu	Ile	Glu 415	Asp
Asn	Glu	Tyr	Thr 420	Ala	Arg	Gln	Gly	Ala 425	Lys	Phe	Pro	Ile	Lys 430	Trp	Thr
Ala	Pro	Glu 435	Ala	Ala	Leu	Tyr	Gly 440	Arg	Phe	Thr	Ile	Lys 445		Asp	Val
Trp	Ser 450	Phe	Gly	Ile	Leu	Leu 455		Glu	Leu	Thr	Thr 460		Gly	Arg	Val
Pro 465	Tyr	Pro	Gly	Met	Val 470	Asn	Arg	Glu	Val	Leu 475		Gln	Val	Glu	Arg 480
Gly	Tyr	Arg	Met	Pro 485		Pro	Pro	Glu	Cys 490		Glu	Ser	Leu	His 495	Asp
Leu	Met	Cys	Gln 500	Cys	Trp	Arg	Lys	Glu 505		Glu	Glu	Arg	Pro 510	Thr	Phe
Glu	Tyr	Leu 515		Ala	Phe	Leu	Glu 520	Asp	Tyr	Phe	Thr	Ser 525		Glu	Pro

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Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
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Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Phe Ser Val
_Val_Pro_Ser_Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
                             120
        115
Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
                        135
Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
                    150
Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Asn Pro Gly
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Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly

			180					185					190			
Ala	Tyr	Ser 195	Leu	Ser	Ile	Arg	Asp 200	Trp	Asp	Glu	Ile	Arg 205	Gly	Asp	Asn	
Val	Lys 210	His	Tyr	Lys	Ile	Arg 215	Lys	Leu	Asp	Asn	Gly 220	Gly	Tyr	Tyr	Ile	
Thr 225	Thr	Arg	Ala	Gln	Phe 230	Asp	Thr	Leu	Gln	Lys 235	Leu	Val	Lys	His	Tyr 240	
Thr	Glu	His	Ala	Asp 245	Gly	Leu	Суз	His	Lys 250	Leu	Thr	Thr	Val	Cys 255	Pro	
Thr	Val	Lys	Pro 260	Gln	Thr	Gln	Gly	Leu 265	Ala	Lys	Asp	Ala	Trp 270	Glu	Ile	
Pro	Arg	Glu 275	Ser	Leu	Arg	Leu	Glu 280	Val	Lys	Leu	Gly	Gln 285	Gly	Cys	Phe	
Gly	Glu 290	Val	Trp	Met	Gly	Thr 295	Trp	Asn	Gly	Thr	Thr 300	Lys	Val	Ala	Ile	
305					310				Pro	315					320	
				325					Asp 330					335		
			340					345	Ile				350			
		355					360		Glu			365				
	370					375			Ala		380					
385	-			_	390		-		His	395					400	
				405					410					415	Gly	
			420					425	•				430		Ala	
		435					440					445			Arg	
	450					455					460				Glu	
465					470					475					Glu 480	
				485					Arg 490					495		
			500					505	Asn				510			
Pro	Asp	Glu	Arg	Pro	Thr	Phe	Glu	Tyr	Ile	Gln	Ser	Phe	Leu	Glu	Asp	

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170

Glu	Ser	Glu	Thr 180	Thr	Lys	Gly	Ala	Tyr 185	Ser	Leu	Ser	Ile	Arg 190	Asp	Trp
Asp	Asp	Met 195	Lys	Gly	Asp	His	Val 200	Lys	His	Tyr	Lys	Ile 205	Arg	ГÄź	Leu
Asp	Asn 210	Gly	Gly	Tyr	Tyr	Ile 215	Thr	Thr	Arg	Ala	Gln 220	Phe	Glu	Thr	Leu
Gln 225	Gln	Leu	Val	Gln	His 230	Tyr	Ser	Glu	Arg	Ala 235	Ala	Gly	Leu	Cys	Cys 240
Arg	Leu	Val	Val	Pro 245	Суѕ	His	Lys	Gly	Met 250	Pro	Arg	Leu	Thr	Asp 255	Leu
Ser	Val	Lys	Thr 260	ГЛЗ	Asp	Val	Trp	Glu 265	Ile	Pro	Arg	Glu	Ser 270	Leu	Gln
Leu	Ile	Lys 275	Arg	Leu	Gly	Asn	Gly 280	Gln	Phe	Gly	Glu	Val 285	Trp	Met	Gly
Thr	Trp 290	Asn	Glу	Asn	Thr	Lys 295	Val	Ala	Ile	Lys	Thr 300	Leu	Lys	Pro	Gly
Thr 305	Met	Ser	Pro	Glu	Ser 310	Phe	Leu	Glu	Glu	Ala 315	Gln	Ile	Met	Lys	Lys 320
Leu	Lys	His	Asp	Lys 325	Leu	Val	Gln	Leu	Tyr 330	Ala	Val	Val	Ser	Glu 335	Glu
Pro	Ile	Tyr	Ile 340	Val	Thr	Glu	Tyr	Met 345	Asn	Lys	Gly	Ser	Leu 350	Leu	Asp
Phe	Leu	Lys 355	_	Gly	Glu	Gly	Arg 360	Ala	Leu	Lys	Leu	Pro 365		Leu	Val
Asp	Met 370	Ala	Ala	Gln	Val	Ala 375	Ala	Gly	Met	Ala	Tyr 380	Ile	Glu	Arg	Met
Asn 385	Tyr	Ile	His	Arg	Asp 390	Leu	Arg	Ser	Ala	Asn 395		Leu	Val	Gly	Asn 400
Gly	Leu	Ile	Cys	Lys 405	Ile	Ala	Asp	Phe	Gly 410		Ala	Arg	Leu	Ile 415	
Asp	Asn	Glu	Tyr 420		Ala	Arg	Gln	Gly 425		Lys	Phe	Pro	11e 430	Lys	Trp
Thr	Ala	Pro 435		Ala	Ala	Leu	Tyr 440	Gly	Arg	Phe	Thr	Ile 445		Ser	Asp
Val	Trp 450		Phe	Gly	Ile	Leu 455		Thr	Glu	Leu	Val 460		Lys	Gly	Arg
Val 465	Pro	Tyr	Pro	Gly	Met 470	Asn	Asn	Arg	Glu	Val 475		Glu	Gln	Val	Glu 480
Arg	Gly	Tyr	Arg	Met 485		Cys	Pro	Gln	Asp 490		Pro	Ile	Ser	Leu 495	
Glu	Leu	Met	Ile 500		Cys	Trp	Lys	Lys 505		Pro	Glu	Glu	Arg 510		Thr

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WO 2005/059168
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Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro

Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly

Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr

Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn

Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala 120

Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln

Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg 150

Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu 170 165

Ser	Glu	Thr	Thr 180	ГЛS	Gly	Ala	Tyr	Ser 185	Leu	Ser	Ile	Arg	Asp 190	Trp	Asp
Glu	Ala	Lys 195	Gly	Asp	His	Val	Lys 200	His	Tyr	Lys	Ile	Arg 205	Lys	Leu	Asp
Ser	Gly 210	Gly	Tyr	Tyr	Ile	Thr 215	Thr	Arg	Ala	Gln	Phe 220	Asp	Thr	Ile	Gln
Gln 225	Leu	Val	Gln	His	Tyr 230	Ile	Glu	Arg	Ala	Ala 235	Gly	Leu	Суз	Cys	Arg 240
Leu	Ala	Val	Pro	Cys 245	Pro	Lys	Gly	Thr	Pro 250	Lys	Leu	Ala	Asp	Leu 255	Ser
Val	Lys	Thr	Lys 260	Asp	Val	Trp	Glu	Ile 265	Pro	Arg	Glu	Ser	Ьеи 270	Gln	Leu
Leu	Gln	Lys 275	Leu	Gly	Asn	Gly	Gln 280	Phe	Gly	Glu	Val	Trp 285	Met	Gly	Thr
Trp	Asn 290	Gly	Thr	Thr	Lys	Val 295	Ala	Val	ГЛЗ	Thr	Leu 300	Lys	Pro	Gly	Thr
Met 305	Ser	Pro	Glu	Ala	Phe 310	Leu	Glu	Glu	Ala	Gln 315	Ile	Met	Lys	Arg	Leu 320
Arg	His	Asp	Lys	Leu 325	Val	Gln	Leu	Tyr	Ala 330	Val	Val	Ser	Glu	Glu 335	Pro
Ile	Tyr	Ile	Val 340	Thr	Glu	Phe	Met	Ser 345	Gln	Gly	Ser	Leu	Leu 350		Phe
Leu	Lys	Asp 355	Gly	Asp	Gly	Arg	Tyr 360	Leu	Lys	Leu	Pro	Gln 365		Val	Asp
Met	Ala 370	Ala	Gln	Ile	Ala	Ala 375	Gly	Met	Ala	Tyr	Ile 380		Arg	Met	Asn
Tyr 385	Ile	His	Arg	Asp	Leu 390	Arg	Ala	Ala	Asn	11e 395		Val	Gly	Asp	Asn 400
Leu	Val	Cys	Lys ·	Ile 405	Ala	Asp	Phe	Gly	Leu 410		Arg	Leu	Ile	Glu 415	Asp
Asn	Glu	Tyr	Thr 420	Ala	Arg	Gln	Gly	Ala 425		Phe	Pro	Ile	Lys 430		Thr
Ala	Pro	Glu 435		Ala	Leu	Phe	Gly 440	Lys	Phe	Thr	Ile	Lys 445		Asp	Val
Trp	Ser 450	Phe	Gly	Ile	Leu	Leu 455		Glu	Leu	Val	Thr 460		Gly	Arg	Val
Pro 465	Tyr	Pro	Gly	Met	Asn 470	Asn	Arg	Glu	Val	Leu 475		Gln	Val	Glu	Arg 480
Gly	Tyr	Arg	Met	Gln 485	Cys	Pro	Gly	Gly	Cys 490		Pro	Ser	Leu	His 495	Asp
Val	Met	Val	Gln 500	Cys	Trp	Lys	Arg	Glu 505		Glu	Glu	Arg	Pro 510		Phe

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro 520 Gln Tyr Gln Pro Gly Asp Asn Gln 530 <210> 41 <211> 529 <212> PRT <213> Homo sapiens <220> <223> Fgr kinase (Fig. 18) <220> <221> SITE <222> (291) <223> Constant amino acid K in domain SH2 <220> <221> SITE <222> (334) <223> Constant amino acid T in domain SH2 <220> <221> SITE <222> (523) <223> Constant amino acid Y in domain SH1 <400> 41 Met Gly Cys Val Phe Cys Lys Leu Glu Pro Val Ala Thr Ala Lys Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala 40 His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile 120 Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr

popia.

165 170 175 Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly 185 Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly 265 Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln 315 Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe 330 Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln 345 Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu 360 Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg 375 Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp 390 . 395 Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe 425 Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys 455 Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro 470

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu

94/103 500 505 510 Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln 520 Thr <210> 42 <211> 525 <212> PRT <213> Homo sapiens <220> <223> Hck kinase (Fig. 18) <220> <221> SITE <222> (289) <223> Constant amino acid K in domain SH2 <220> <221> SITE <222> (332) <223> Constant amino acid T in domain SH2 <220> <221> SITE

<222> (525)

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Arg Ala Pro Arg Met Gly Cys Met Lys Ser Lys Phe Leu Gln Val Gly
20 25 30

Gly Asn Thr Phe Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro 35 40 45

Val Tyr Val Pro Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser 50 55 60

His Asn Ser Asn Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile 65 70 75 80

Ile Val Val Ala Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu 85 90 95

Ser Phe Gln Lys Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu 100 105 110

Trp Trp Lys Ala Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro 115 120 125

Ser Asn Tyr Val Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe 130 135 140

Phe Lys Gly Ile Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro 145 150 155 160

Gly	Asn	Met	Leu	Gly 165	Ser	Phe	Met	Ile	Arg 170	Asp	Ser	Glu	Thr	Thr 175	Lys
Gly	Ser	Tyr	Ser 180	Leu	Ser	Val	Arg	Asp 185	Tyr	Asp	Pro	Arg	Gln 190	Gly	Asp
Thr	Val	Lys 195	His	Tyr	Lys	Ile	Arg 200	Thr	Leu	Asp	Asn	Gly 205	Gly	Phe	Tyr
Ile	Ser 210	Pro	Arg	Ser	Thr	Phe 215	Ser	Thr	Leu	Gln	Glu 220	Leu	Val	Asp	His
Tyr 225	Lys	Lys	Gly	Asn	Asp 230	Gly	Leu	Cys	Gln	Lys 235	Leu	Ser	Val	Pro	Cys 240
Met	Ser	Ser	Lys	Pro 245	Gln	Lys	Pro	Trp	Glu 250	Lys	Asp	Ala	Trp	Glu 255	Ile
Pro	Arg	Glu	Ser 260	Leu	Lys	Leu	Glu	Lys 265	ГÀЗ	Leu	Gly	Ala	Gly 270	Gln	Phe
Gly	Glu	Val 275	Trp	Met	Ala	Thr	Tyr 280	Asn	Lys	His	Thr	Lys 285	Val	Ala	Val
Lys	Thr 290	Met	Lys	Pro	Gly	Ser 295	Met	Ser	Val	Glu	Ala 300	Phe	Leu	Ala	Glu
Ala 305	Asn	Val	Met	ГÀЗ	Thr 310	Leu	Gln	His	Asp	Lys 315	Leu	Val	Lys	Leu	His 320
Ala	Val	Val	Thr	Lys 325	Glu	Pro	Ile	Tyr	11e 330	Ile	Thr	Glu	Phe	Met 335	Ala
	Gly		340					345					350		
Pro	Leu	Pro 355	Lys	Leu	Ile	Asp	Phe 360	Ser	Ala	Gln	Ile	Ala 365	Glu	Gly	Met
	Phe 370				_	375	_			_	380				
Asn 385	Ile	Leu	Val	Ser	Ala 390	Ser	Leu	Val	Суз	Lys 395	Ile	Ala	Asp	Phe	Gly 400
Leu	Ala	Arg	Val	Ile 405	Glu	Asp	Asn	Glu	Tyr 410	Thr	Ala	Arg	Glu	Gly 415	Ala
Lys	Phe	Pro	Ile 420	Lys	Trp	Thr	Ala	Pro 425	Glu	Ala	Ile	Asn	Phe 430	Gly	Ser
Phe	Thr	Ile 435	Lys	Ser	Asp	Val	Trp 440	Ser	Phe	Gly	Ile	Leu 445	Leu	Met	Glu
Ile	Val 450	Thr	Tyr	Gly	Arg	Ile 455	Pro	Tyr	Pro	Gly	Met 460	Ser	Asn	Pro	Glu
Val 465	Ile	Arg	Ala	Leu	Glu 470	Arg	Gly	Tyr	Arg	Met 475	Pro	Arg	Pro	Glu	Asn 480
Cys	Pro	Glu	Glu	Leu 485	Tyr	Asn	Ile	Met	Met 490	Arg	Cys	Trp	Lys	Asn 495	Arg

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Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro 515 520 525

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Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu 130 135 140

Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr 145 150 155 160

Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
165 170 175

Gly	Asp	Val	Ile 180	Lys	His	Tyr	Lys	Ile 185	Arg	Ser	Leu	Asp	Asn 190	Gly	Gly
Tyr	Tyr	Ile 195	Ser	Pro	Arg	Ile	Thr 200	Phe	Pro	Cys	Ile	Ser 205	Asp	Met	Ile
Lys	His 210	Tyr	Gln	Lys	Gln	Ala 215	Asp	Gly	Leu	Cys	Arg 220		Leu	Glu	Lys
Ala 225	Cys	Ile	Ser	Pro	Lys 230	Pro	Gln	Lys	Pro	Trp 235	Asp	Lys	Asp	Ala	Trp 240
Glu	Ile	Pro	Arg	Glu 245	Ser	Ile	Lys	Leu	Val 250	Lys	Arg	Leu	Gly	Ala 255	Gly
Gln	Phe	Gly	Glu 260	Val	Trp	Met	Gly	Tyr 265	Tyr	Asn	Asn	Ser	Thr 270	Lys	Val
Ala	Val	Lys 275	Thr	Leu	Ьýз	Pro	Gly 280	Thr	Met	Ser	Val	Gln 285	Ala	Phe	Leu
Glu	Glu 290	Ala	Asn	Leu	Met	Lys 295	Thr	Leu	Gln	His	Asp 300	Lys	Leu	Val	Arg
Leu 305	Tyr	Ala	Val	Val	Thr 310	Arg	Glu	Glu	Pro	Ile 315	Tyr	Ile	Ile	Thr	Glu 320
Tyr	Met	Ala	Lys	Gly 325	Ser	Leu	Leu	Asp	Phe 330	Leu	ГÀЗ	Ser	Asp	Glu 335	Gly
Gly	Lys	Val	Leu 340	Leu	Pro	Lys	Leu	Ile 345	Asp	Phe	Ser	Ala	Gln 350	Ile	Ala
Glu	Gly	Met 355	Ala	Tyr	Ile	Glu	Arg 360	Lys	Asn	Tyr	Ile	His 365	Arg	Asp	Leu
Arg	Ala 370	Ala	Asn	Val		Val 375	Ser	Glu	Ser	Leu	Met 380	Cys	Lys	Ile	Ala
Asp 385	Phe	Gly	Leu	Ala	Arg 390	Val	Ile	Glu	Asp	Asn 395	Glu	Tyr	Thr	Ala	Arg
Glu	Gly	Ala	Lys	Phe 405	Pro	Ile	Lys	Trp	Thr 410	Ala	Pro	Glu	Ala	Ile 415	Asn
Phe	Gly	Суз	Phe 420	Thr	Ile	ГÀЗ	Ser	Asp 425	Val	Trp	Ser	Pho	Gly 430	Ile	Leu
Leu	Tyr	Glu 435	Ile	Val	Thr	Tyr	Gly 440	Lys	Ile	Pro	Tyr	Pro 445		Arg	Thr
Asn	Ala 450	Asp	Val	Met	Thr	Ala 455	Leu	Ser	Gln	Gly	Tyr 460	Arg	Met	Pro	Arg
Val 465	Glu	Asn	Cys	Pro	Asp 470	Glu	Leu	Tyr	Asp	Ile 475	Met	Lys	Met	Cys	Trp 480
Lys	Glu	Lys	Ala	Glu 485	Glu	Arg	Pro	Thr	Phe 490	Asp	Tyr	Leu	Gln	Ser 495	Val
Leu	Asp	Asp	Phe 500	Tyr	Thr	Ala	Thr	Glu 505		Gln	Tyr	Gln	Gln 510	Gln	Pro

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<213> Homo sapiens
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<222> (273)
<223> Constant amino acid K in domain SH2
<220>
<221> SITE
<222> (316)
<223> Constant amino acid T in domain SH2
<220>
<221> SITE
<222> (505)
<223> Constant amino acid Y in domain SH1
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Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
Gly Phe Glu Lys Gly Glu Pro Leu Arg Ile Leu Glu Gln Ser Gly Glu
Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
                            . 105
Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
                            120
Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
                                        155
Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr
Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
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200 195 205 Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys 215 Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr Ala Val Val Thr Glu Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met 345 Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala 390 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro

505

<210> 45 <211> 505 <212> PRT

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<220>
<223> Blk kinase (Fig. 18)
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<221> SITE
<222> (269)
<223> Constant amino acid K in domain SH2
<220>
<221> SITE
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<223> Constant amino acid T in domain SH2
<220>
<221> SITE
<222> (501)
<223> Constant amino acid Y in domain SH1
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Glu Lys Asp Lys Gly Gln Trp Ser Pro Leu Lys Val Ser Ala Gln Asp
Lys Asp Ala Pro Pro Leu Pro Pro Leu Val Val Phe Asn His Leu Thr
                             40
Pro Pro Pro Pro Asp Glu His Leu Asp Glu Asp Lys His Phe Val Val
Ala Leu Tyr Asp Tyr Thr Ala Met Asn Asp Arg Asp Leu Gln Met Leu
Lys Gly Glu Lys Leu Gln Val Leu Lys Gly Thr Gly Asp Trp Trp Leu
Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe
                                105
Val Ala Arg Val Glu Ser Leu Glu Met Glu Arg Trp Phe Phe Arg Ser
                            120
Gln Gly Arg Lys Glu Ala Glu Arg Gln Leu Leu Ala Pro Ile Asn Lys
                        135
Ala Gly Ser Phe Leu Ile Arg Glu Ser Glu Thr Asn Lys Gly Ala Phe
Ser Leu Ser Val Lys Asp Val Thr Thr Gln Gly Glu Leu Ile Lys His
                                    170
Tyr Lys Ile Arg Cys Leu Asp Glu Gly Gly Tyr Tyr Ile Ser Pro Arg
                                185
Ile Thr Phe Pro Ser Leu Gln Ala Leu Val Gln His Tyr Ser Lys Lys
Gly Asp Gly Leu Cys Gln Arg Leu Thr Leu Pro Cys Val Arg Pro Ala
    210
                        215
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Pro 225	Gln	Asn	Pro	Trp	Ala 230	Gln	Asp	Glu	Trp	Glu 235	Ile	Pro	Arg	Gln	Ser 240
Leu	Arg	Leu	Val	Arg 245	Lys	Leu	Gly	Ser	Gly 250	Gln	Phe	Gly	Glu	Val 255	Trp
Met	Gly	Tyr	Tyr 260	Lys	Asn	Asn	Met	Lys 265	Val	Ala	Ile	Lys	Thr 270	Leu	Lys
Glu	Gly	Thr 275	Met	Ser	Pro	Glu	Ala 280	Phe	Leu	Gly	Glu	Ala 285	Asn	Met	Met
Lys	Ala 290	Leu	Gln	His	Glu	Arg 295	Leu	Val	Arg	Leu	Tyr 300	Ala	Val	Val	Thr
305					310			Glu		315					320
Leu	Asp	Phe	Leu	Lys 325	Thr	Asp	Glu	Gly	Ser 330	Arg	Leu	Ser	Leu	Pro 335	Arg
Leu	Ile	Asp	Met 340	Ser	Ala	Gln	Ile	Ala 345	Glu	Gly	Met	Ala	Tyr 350	Ile	Glu
		355					360					365			Val
	370					375					380				Ile
385					390			Glu		395					400
				405				Phe	410					415	
Asp	Val	Trp	Ser 420	Phe	Gly	Val	Leu	Leu 425		Glu	Val	Val	Thr 430	Tyr	Gly
Arg	Val	Pro 435		Pro	Gly	Met	Ser 440		Pro	Glu	Val	Ile 445		Asn	Leu
Glu	Arg 450	Gly	Tyr	Arg	Met	Pro 455		Pro	Asp	Thr	Cys 460		Pro	Glu	Leu
Tyr 465	Arg	Gly	Val	Ile	Ala 470		Cys	Trp	Arg	Ser 475		Pro	Glu	Glu	Arg 480
Pro	Thr	Phe	Glu	Phe 485		Gln	Ser	Val	Leu 490		Asp	Phe	Tyr	Thr 495	Ala
Thr	Glu	Arg	Gln 500		Glu	Leu	Gln	Pro 505							

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 Oligonucleotide (sense) used for the generation of

## 102/103

Src-K298A (page 35 of description)

<400> 46 ccagggtggc catcgccacc ctgaagcctg gcac	34
<210> 47 <211> 34 <212> DNA <213> Artificial Sequence	-
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<210> 48 <211> 32 <212> DNA <213> Artificial Sequence	
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<210> 50 <211> 29 <212> DNA <213> Artificial Sequence	
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## 103/103

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 generation of Src-Y530F (page 35 of description)

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